

SEQUENCE LISTING

<110> Bisgard-Frantzen, Henrik
Pedersen, Sven
Svendsen, Allan

<120> Fungamyl-like Alpha-Amylase Variants

<130> 5835.210-US

<140> US 09/710,339

<141> 2000-11-09

<150> US 60/165,786

<151> 1999-11-16

<160> 7

<170> PatentIn version 3.2

<210> 1

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<212> DNA

<213> Aspergillus Oryzae

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Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala Pro
-15 -10 -5

gct ttg gct gca acg cct gcg gac tgg cga tcg caa tcc att tat ttc 152
Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe
-1 1 5 10

ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg act 200
Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr
15 20 25

tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc atc 248
Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile
30 35 40 45

atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc tgg 296

Ile	Asp	Lys	Leu	Asp	Tyr	Ile	Gln	Gly	Met	Gly	Phe	Thr	Ala	Ile	Trp		
				50					55					60			
atc	acc	ccc	gtt	aca	gcc	cag	ctg	ccc	cag	acc	acc	gca	tat	gga	gat	344	
Ile	Thr	Pro	Val	Thr	Ala	Gln	Leu	Pro	Gln	Thr	Thr	Ala	Tyr	Gly	Asp		
			65					70					75				
gcc	tac	cat	ggc	tac	tgg	cag	cag	gat	ata	tac	tct	ctg	aac	gaa	aac	392	
Ala	Tyr	His	Gly	Tyr	Trp	Gln	Gln	Asp	Ile	Tyr	Ser	Leu	Asn	Glu	Asn		
		80					85					90					
tac	ggc	act	gca	gat	gac	ttg	aag	gcg	ctc	tct	tcg	gcc	ctt	cat	gag	440	
Tyr	Gly	Thr	Ala	Asp	Asp	Leu	Lys	Ala	Leu	Ser	Ser	Ala	Leu	His	Glu		
	95					100					105						
agg	ggg	atg	tat	ctt	atg	gtc	gat	gtg	gtt	gct	aac	cat	atg	ggc	tat	488	
Arg	Gly	Met	Tyr	Leu	Met	Val	Asp	Val	Val	Ala	Asn	His	Met	Gly	Tyr		
110					115					120					125		
gat	gga	gcg	ggt	agc	tca	gtc	gat	tac	agt	gtg	ttt	aaa	ccg	ttc	agt	536	
Asp	Gly	Ala	Gly	Ser	Ser	Val	Asp	Tyr	Ser	Val	Phe	Lys	Pro	Phe	Ser		
				130					135					140			
tcc	caa	gac	tac	ttc	cac	ccg	ttc	tgt	ttc	att	caa	aac	tat	gaa	gat	584	
Ser	Gln	Asp	Tyr	Phe	His	Pro	Phe	Cys	Phe	Ile	Gln	Asn	Tyr	Glu	Asp		
			145					150					155				
cag	act	cag	gtt	gag	gat	tgc	tgg	cta	gga	gat	aac	act	gtc	tcc	ttg	632	
Gln	Thr	Gln	Val	Glu	Asp	Cys	Trp	Leu	Gly	Asp	Asn	Thr	Val	Ser	Leu		
			160				165					170					
cct	gat	ctc	gat	acc	acc	aag	gat	gtg	gtc	aag	aat	gaa	tgg	tac	gac	680	
Pro	Asp	Leu	Asp	Thr	Thr	Lys	Asp	Val	Val	Lys	Asn	Glu	Trp	Tyr	Asp		
	175					180					185						
tgg	gtg	gga	tca	ttg	gta	tcg	aac	tac	tcc	att	gac	ggc	ctc	cgt	atc	728	
Trp	Val	Gly	Ser	Leu	Val	Ser	Asn	Tyr	Ser	Ile	Asp	Gly	Leu	Arg	Ile		
190					195					200					205		
gac	aca	gta	aaa	cac	gtc	cag	aag	gac	ttc	tgg	ccc	ggg	tac	aac	aaa	776	
Asp	Thr	Val	Lys	His	Val	Gln	Lys	Asp	Phe	Trp	Pro	Gly	Tyr	Asn	Lys		
				210					215					220			
gcc	gca	ggc	gtg	tac	tgt	atc	ggc	gag	gtg	ctc	gac	ggt	gat	ccg	gcc	824	
Ala	Ala	Gly	Val	Tyr	Cys	Ile	Gly	Glu	Val	Leu	Asp	Gly	Asp	Pro	Ala		
			225					230					235				
tac	act	tgt	ccc	tac	cag	aac	gtc	atg	gac	ggc	gta	ctg	aac	tat	ccc	872	
Tyr	Thr	Cys	Pro	Tyr	Gln	Asn	Val	Met	Asp	Gly	Val	Leu	Asn	Tyr	Pro		
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att	tac	tat	cca	ctc	ctc	aac	gcc	ttc	aag	tca	acc	tcc	ggc	agc	atg	920	
Ile	Tyr	Tyr	Pro	Leu	Leu	Asn	Ala	Phe	Lys	Ser	Thr	Ser	Gly	Ser	Met		
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gac	gac	ctc	tac	aac	atg	atc	aac	acc	gtc	aaa	tcc	gac	tgt	cca	gac	968	
Asp	Asp	Leu	Tyr	Asn	Met	Ile	Asn	Thr	Val	Lys	Ser	Asp	Cys	Pro	Asp		

270	275	280	285	
tca aca ctc ctg ggc aca ttc gtc gag aac cac gac aac cca cgg ttc				1016
Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe				
	290	295	300	
gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca ttc				1064
Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe				
	305	310	315	
atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa cag				1112
Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln				
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cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg ctc				1160
His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu				
	335	340	345	
tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc gcg				1208
Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala				
	350	355	360	365
aac gca atc cgg aac tat gcc att agc aaa gat aca gga ttc gtg acc				1256
Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr				
	370	375	380	
tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg cgc				1304
Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg				
	385	390	395	
aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag ggt				1352
Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly				
	400	405	410	
gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac aca				1400
Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr				
	415	420	425	
gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg gtt				1448
Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val				
	430	435	440	445
ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct agg				1496
Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg				
	450	455	460	
gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt agc				1544
Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser				
	465	470	475	
tcg tgaagggtgg agagtatatg atggtactgc tattcaatct ggcattggac				1597
Ser				
agtgagtttg agtttgatgt acagttggag tcgttactgc tgtcatcccc ttatactctt				1657
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1734

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Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
15 20 25

Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
30 35 40

Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
45 50 55 60

Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
65 70 75

Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
80 85 90

Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
95 100 105

Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
110 115 120

Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
125 130 135 140

Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
145 150 155

Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
160 165 170

Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
175 180 185

Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
190 195 200

Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
205 210 215 220

Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
225 230 235

Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
240 245 250

Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
255 260 265

Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
270 275 280

Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
285 290 295 300

Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
305 310 315

Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
320 325 330

Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
335 340 345

Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
350 355 360

Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
365 370 375 380

Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
385 390 395

Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
400 405 410

Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
415 420 425

Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
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Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
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Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
465 470 475

Ser Ser

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